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FIGURE 1A

Map of a First IL-17 Receptor Like cDNA (SEQ ID No: 1) and Amino Acid (SEQ ID NO: 2)

#5

```
  1 ATAAAAGCGCAGCGTGCGGGTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60
                                                    M  S  L  V  -

 61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
     L  L  S  L  A  A  L  C  R  S  A  V  P  R  E  P  T  V  Q  C  -

121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
     G  S  E  T  G  P  S  P  E  W  M  L  Q  H  D  L  I  P  G  D  -

181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACAGGGGACTATTCAAT 240
     L  R  D  L  R  V  E  P  V  T  T  S  V  A  T  G  D  Y  S  I  -

241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCAC 300
     L  M  N  V  S  W  V  L  R  A  D  A  S  I  R  L  L  K  A  T  -

301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTA 360
     K  I  C  V  T  G  K  S  N  F  Q  S  Y  S  C  V  R  C  N  Y  -

361 CACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACAT 420
     T  E  A  F  Q  T  Q  T  R  P  S  G  G  K  W  T  F  S  Y  I  -

421 CGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCCATAATATTCCTAATGC 480
     G  F  P  V  E  L  N  T  V  Y  F  I  G  A  H  N  I  P  N  A  -

481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTCACCAGGCTGCCTAGA 540
     N  M  N  E  D  G  P  S  M  S  V  N  F  T  S  P  G  C  L  D  -

541 CCACATAATGAAATATAAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACAT 600
     H  I  M  K  Y  K  K  K  C  V  K  A  G  S  L  W  D  P  N  I  -

601 CACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCACAACCACTCCCCTGGG 660
     T  A  C  K  K  N  E  E  T  V  E  V  N  F  T  T  T  P  L  G  -

661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGA 720
     N  R  Y  M  A  L  I  Q  H  S  T  I  I  G  F  S  Q  V  F  E  -

721 GCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGA 780
     P  H  Q  K  K  Q  T  R  A  S  V  V  I  P  V  T  G  D  S  E  -

781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACA 840
     G  A  T  V  Q  L  T  P  Y  F  P  T  C  G  S  D  C  I  R  H  -

841 TAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAA 900
     K  G  T  V  V  L  C  P  Q  T  G  V  P  F  P  L  D  N  N  K  -

901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGT 960
     S  K  P  G  G  W  L  P  L  L  L  L  S  L  L  V  A  T  W  V  -
```

Figure 1B

```
 961 GCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTC 1020
      L  V  A  G  I  Y  L  M  W  R  H  E  R  I  K  K  T  S  F  S  -

1021 TACCACCACACTACTGCCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTT 1080
      T  T  T  L  L  P  P  I  K  V  L  V  V  Y  P  S  E  I  C  F  -

1081 CCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCAT 1140
      H  H  T  I  C  Y  F  T  E  F  L  Q  N  H  C  R  S  E  V  I  -

1141 CCTCGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCAC 1200
      L  E  K  W  Q  K  K  K  I  A  E  M  G  P  V  Q  W  L  A  T  -

1201 TCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTG 1260
      Q  K  K  A  A  D  K  V  V  F  L  L  S  N  D  V  N  S  V  C  -

1261 CGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCC 1320
      D  G  T  C  G  K  S  E  G  S  P  S  E  N  S  Q  D  L  F  P  -

1321 CCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGT 1440
      L  A  F  N  L  F  C  S  D  L  R  S  Q  I  H  L  H  K  Y  V  -

1441 GGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCC 1500
      V  V  Y  F  R  E  I  D  T  K  D  D  Y  N  A  L  S  V  C  P  -

1501 CAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCA 1560
      K  Y  H  L  M  K  D  A  T  A  F  C  A  E  L  L  H  V  K  Q  -

1561 GCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCC 1620
      Q  V  S  A  G  K  R  S  Q  A  C  H  D  G  C  C  S  L  *

1621 CACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAAC 1680

1681 GTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTT 1740

1741 TATACCAATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAAC 1800

1801 TACATTTACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAA 1860

1861 CTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCAGC                     1901
```

FIGURE 2

Homology of a First IL-17 human Receptor Like Polypeptide Amino Acid Seqeunce (SEQ ID NO: 2) and Known Human IL-17 Receptor Family Member (SEQ ID NO: 3)

FIGURE 3A

Map of a Second Human IL-17 Receptor Like cDNA (SEQ ID NO: 4) And Amino Acid (SEQ ID NO: 5) Sequences

```
1 ATAAAAGCGC AGCGTGCGGG TGGCCTGGAT CCCGCGCAGT GGCCCGGCGA TGTCGCTCGT 60
                                                    M  S  L  V  -

61 GCTGCTAAG CCTGGCCGCG CTGTGCAGGA GCGCCGTACC CCGAGAGCCG ACCGTTCAATG 120
    L  L  S  L  A  A  L  C  R  S  A  V  P  R  E  P  T  V  Q  C  -

121 TGGCTCTGA AACTGGGCCA TCTCCAGAGT GGATGCTACA ACATGATCTA ATCCCCGGAGA 180
    G  S  E  T  G  P  S  P  E  W  M  L  Q  H  D  L  I  P  G  D  -

181 CTTGAGGGA CCTCCGAGTA GAACCTGTTA CAACTAGTGT TGCAACAGGG GACTATTCAAT 240
    L  R  D  L  R  V  E  P  V  T  T  S  V  A  T  G  D  Y  S  I  -

241 TTTGATGAA TGTAAGCTGG GTACTCCGGG CAGATGCCAG CATCCGCTTG TTGAAGGCCAC 300
    L  M  N  V  S  W  V  L  R  A  D  A  S  I  R  L  L  K  A  T  -

301 CAAGATTTG TGTGACGGGC AAAAGCAACT TCCAGTCCTA CAGCTGTGTG AGGCTGGAGTG 360
    K  I  C  V  T  G  K  S  N  F  Q  S  Y  S  C  V  R  L  E  C  -

361 CAGTGGTGC GATCATGGCT CGCTGCGACC TCAATCTTCT GGGCTCAAGC GATCGTTCTGC 420
    S  G  A  I  M  A  R  C  D  L  N  L  L  G  S  S  D  R  S  A  -

421 TTCAGCCTC CCGAGCGGCT GGGACTGCAG GCGTGGGCCA CCAGACCTGG CTAATTTTTGT 480
    S  A  S  R  A  A  G  T  A  G  V  G  H  Q  T  W  L  I  F  V  -

481 AGTTTTTGT AGAGGGGGGT TTCACCGTGT TGCTGGTCTT GAATTCCAGT GCTCAGGCGAT 540
    V  F  V  E  G  G  F  T  V  L  L  V  L  N  S  S  A  Q  A  I  -

541 CTGCCTGCC TCGGCTTCCC AAAGTGCTGG GATTACAGTG GACATTTTCC TACATCGGCTT 600
    C  L  P  R  L  P  K  V  L  G  L  Q  W  T  F  S  Y  I  G  F  -

601 CCCTGTAGA GCTGAACACAGT CTATTTCATT GGGGCCCATA ATATTCCTAA TGCAAATAT 660
    P  V  E  L  N  T  V  Y  F  I  G  A  H  N  I  P  N  A  N  M  -

661 GAATGAAGA TGGCCCTTCCAT GTCTGTGAAT TTCACCTCAC CAGGCTGCCT AGACCACAT 720
    N  E  D  G  P  S  M  S  V  N  F  T  S  P  G  C  L  D  H  I  -

721 AATGAAATA TAAAAAAAAG TGTGTCAAGG CCGGAAGCCT GTGGGATCCG AACATCACTGC 780
    M  K  Y  K  K  K  C  V  K  A  G  S  L  W  D  P  N  I  T  A  -

781 TTGTAAGAA GAATGAGGAG ACAGTAGAAG TGAACTTCAC AACCACTCCC CTGGGAAACAG 840
    C  K  K  N  E  E  T  V  E  V  N  F  T  T  T  P  L  G  N  R  -

841 ATACATGGC TCTTATCCAA CACAGCACTA TCATCGGGTT TTCTCAGGTG TTTGAGCCACA 900
    Y  M  A  L  I  Q  H  S  T  I  I  G  F  S  Q  V  F  E  P  H  -

901 CCAGAAGAA ACAAACGCGA GCTTCAGTGG TGATTCCAGT GACTGGGGAT AGTGAAGGTGC 960
    Q  K  K  Q  T  R  A  S  V  V  I  P  V  T  G  D  S  E  G  A  -

961 TACGGTGCA GCTGACTCCA TATTTTCCTA CTTGTGGCAG CGACTGCATC CGACATAAAGG 1020
    T  V  Q  L  T  P  Y  F  P  T  C  G  S  D  C  I  R  H  K  G  -
```

Figure 3B

```
1021 AACAGTTGT GCTCTGCCCACA AACAGGCGTCCC TTTCCCTCTGGA TAACAACAAAAG CAA 1080
      T  V  V  L  C  P  Q  T  G  V  P  F  P  L  D  N  N  K  S  K  -

1081 GCCGGGAGG CTGGCTGCCTCT CCTCCTGCTGTC TCTGCTGGTGGC CACATGGGTGCT GGT 1140
      P  G  G  W  L  P  L  L  L  L  S  L  L  V  A  T  W  V  L  V  -

1141 GGCAGGGAT CTATCTAATGTG GAGGCACGAAAG GATCAAGAAGAC TTCCTTTTCTAC CAC 1200
      A  G  I  Y  L  M  W  R  H  E  R  I  K  K  T  S  F  S  T  T  -

1201 CACACTACT GCCCCCCATTAA GGTTCTTGTGGT TTACCCATCTGA AATATGTTTCCA TCA 1260
      T  L  L  P  P  I  K  V  L  V  V  Y  P  S  E  I  C  F  H  H  -

1261 CACAATTTG TTACTTCACTGA ATTTCTTCAAAA CCATTGCAGAAG TGAGGTCATCCT CGA 1320
      T  I  C  Y  F  T  E  F  L  Q  N  H  C  R  S  E  V  I  L  E  -

1321 AAAGTGGCA GAAAAAGAAAAT AGCAGAGATGGG TCCAGTGCAGTG GCTTGCCACTCA AAA 1380
      K  W  Q  K  K  K  I  A  E  M  G  P  V  Q  W  L  A  T  Q  K  -

1381 GAAGGCAGC AGACAAAGTCGT CTTCCTTCTTTC CAATGACGTCAA CAGTGTGTGCGA TGG 1440
      K  A  A  D  K  V  V  F  L  L  S  N  D  V  N  S  V  C  D  G  -

1441 TACCTGTGG CAAGAGCGAGGG CAGTCCCAGTGA GAACTCTCAAGA CCTCTTCCCCCT TGC 1500
      T  C  G  K  S  E  G  S  P  S  E  N  S  Q  D  L  F  P  L  A  -

1501 CTTTAACCT TTTCTGCAGTGA TCTAAGAAGCCA GATTCATCTGCA CAAATACGTGGT GGT 1560
      F  N  L  F  C  S  D  L  R  S  Q  I  H  L  H  K  Y  V  V  V  -

1561 CTACTTTAG AGAGATTGATAC AAAAGACGATTA CAATGCTCTCAG TGTCTGCCCCAA GTA 1620
      Y  F  R  E  I  D  T  K  D  D  Y  N  A  L  S  V  C  P  K  Y  -

1621 CCACCTCAT GAAGGATGCCAC TGCTTTCTGTGC AGAACTTCTCCA TGTCAAGCAGCA GGT 1680
      H  L  M  K  D  A  T  A  F  C  A  E  L  L  H  V  K  Q  Q  V  -

1681 GTCAGCAGG AAAAAGATCACA AGCCTGCCACGA TGGCTGCTGCTC CTTGTAGCCCAC CCA 1740
      S  A  G  K  R  S  Q  A  C  H  D  G  C  C  S  L  *

1741 TGAGAAGCA AGAGACCTTAAA GGCTTCCTATCC CACCAATTACAG GGAAAAAACGTG TGA 1800

1801 TGATCCTGA AGCTTACTATGC AGCCTACAAACA GCCTTAGTAATT AAAACATTTTAT ACC 1860

1861 AATAAAATT TTCAAATATTGC TAACTAATGTAG CATTAACTAACG ATTGGAAACTAC ATT 1920

1921 TACAACTTC AAAGCTGTTTTA TACATAGAAATC AATTACAGCTTT AATTGAAAACTG TAA 1980

1981 CCATTTTGA TAATGCAACAAT AAAGCATCTTCA GC                              2015
```

FIGURE 4

Homology of a Second IL-17 Human Receptor Like Polypeptide AMino Acid Sequence (SEQ ID No: 5) and KNown Human IL_17 Receptor Family Mamber (SEQ ID NO: 3)

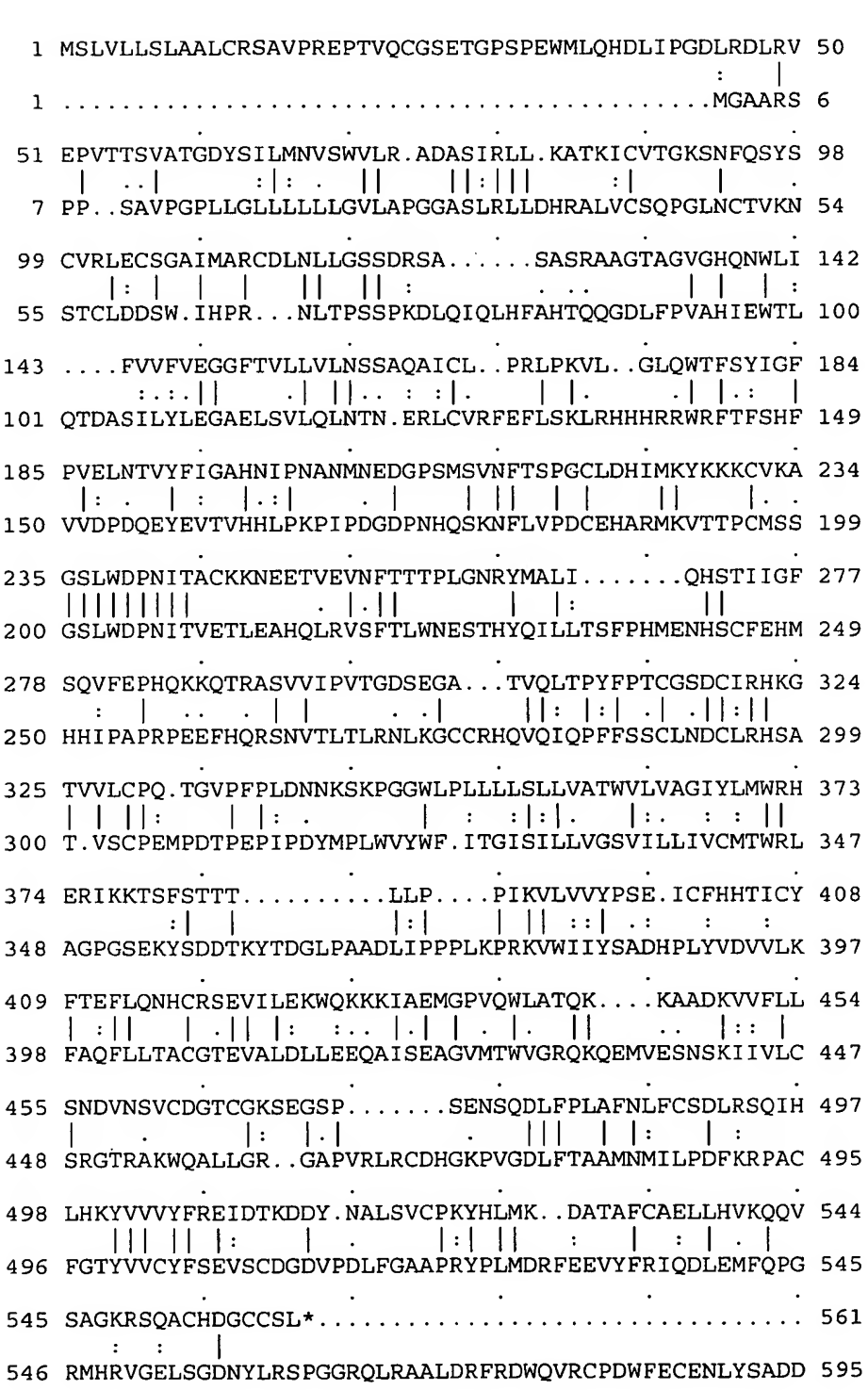

FIGURE 5A
Map of a Third IL-17 Receptor Like cDNA (SEQ ID NO: 6) and Amino Acid (SEQ ID NO: 7) Sequence

```
   1 ATAAAAGCGCAGCGTGCGGGTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT  60

  61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120

 121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGGAGA 180

 181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACAGGGGACTATTCAAT 240

 241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCCTACATCGGCTTCC 300
                                     M  W  T  F  S  Y  I  G  F  P  -

 301 CTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCCATAATATTCCTAATGCAAATATGA 360
       V  E  L  N  T  V  Y  F  I  G  A  H  N  I  P  N  A  N  M  N  -

 361 ATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTCACCAGGCTGCCTAGACCACATAA 420
       E  D  G  P  S  M  S  V  N  F  T  S  P  G  C  L  D  H  I  M  -

 421 TGAAATATAAAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTT 480
       K  Y  K  K  K  C  V  K  A  G  S  L  W  D  P  N  I  T  A  C  -

 481 GTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCACAACCACTCCCCTGGGAAACAGAT 540
       K  K  N  E  E  T  V  E  V  N  F  T  T  T  P  L  G  N  R  Y  -

 541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACC 600
       M  A  L  I  Q  H  S  T  I  I  G  F  S  Q  V  F  E  P  H  Q  -

 601 AGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTA 660
       K  K  Q  T  R  A  S  V  V  I  P  V  T  G  D  S  E  G  A  T  -

 661 CGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720
       V  Q  L  T  P  Y  F  P  T  C  G  S  D  C  I  R  H  K  G  T  -

 721 CAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGC 780
       V  V  L  C  P  Q  T  G  V  P  F  P  L  D  N  N  K  S  K  P  -

 781 CGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGG 840
       G  G  W  L  P  L  L  L  L  S  L  L  V  A  T  W  V  L  V  A  -

 841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900
       G  I  Y  L  M  W  R  H  E  R  I  K  K  T  S  F  S  T  T  T  -

 901 CACTACTGCCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960
       L  L  P  P  I  K  V  L  V  V  Y  P  S  E  I  C  F  H  H  T  -

 961 CAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTCGAAA 1020
       I  C  Y  F  T  E  F  L  Q  N  H  C  R  S  E  V  I  L  E  K  -

1021 AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGA 1080
       W  Q  K  K  K  I  A  E  M  G  P  V  Q  W  L  A  T  Q  K  K  -

1081 AGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140
       A  A  D  K  V  V  F  L  L  S  N  D  V  N  S  V  C  D  G  T  -

1141 CCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCT 1200
       C  G  K  S  E  G  S  P  S  E  N  S  Q  D  L  F  P  L  A  F  -
```

Figure 5B

```
1201 TTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCT 1260
       N  L  F  C  S  D  L  R  S  Q  I  H  L  H  K  Y  V  V  V  Y  -

1261 ACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACC 1320
       F  R  E  I  D  T  K  D  D  Y  N  A  L  S  V  C  P  K  Y  H  -

1321 ACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGT 1380
       L  M  K  D  A  T  A  F  C  A  E  L  L  H  V  K  Q  Q  V  S  -

1381 CAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCATG 1440
       A  G  K  R  S  Q  A  C  H  D  G  C  C  S  L  *

1441 AGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATG 1500

1501 ATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAA 1560

1561 TAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTA 1620

1621 CAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACC 1680

1681 ATTTTGATAATGCAACAATAAAGCATCTTCAGC                              1713
```

FIGURE 6

Homology of a Third Human IL-17 Receptor Like Polypeptide Amino Acid Sequence (SEQ ID NO: 7) and Known Human IL-17 Receptor Family Member (SEQ ID NO: 3)

FIGURE 7

Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2), Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17 Receptor Like Polypeptides

```
  1  MSLVLLSLAA LCRSAVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
  1  MSLVLLSLAA LCRSAVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV

 51  EPVTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV
 51  EPVTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV

101  RCNYTEAFQT QTRPSGGK-- ---------- ---------- ----------
101  RLECSGAIMA RCDLNLLGSS DRSASASRAA GTAGVGHQNW LIFVVFVEGG

119  ---------- ---------- ------WTFS YIGFPVELNT VYFIGAHNIP
151  FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP
  1                              MWTFS YIGFPVELNT VYFIGAHNIP

143  NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE
201  NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE
 26  NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE

193  TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD
251  TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD
 76  TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD

243  SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVPFPLDN NKSKPGGWLP
301  SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVPFPLDN NKSKPGGWLP
126  SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVPFPLDN NKSKPGGWLP

293  LLLLSLLVAT WVLVAGIYLM WRHERIKKTS FSTTTLLPPI KVLVVYPSEI
351  LLLLSLLVAT WVLVAGIYLM WRHERIKKTS FSTTTLLPPI KVLVVYPSEI
176  LLLLSLLVAT WVLVAGIYLM WRHERIKKTS FSTTTLLPPI KVLVVYPSEI

343  CFHHTICYFT EFLQNHCRSE VILEKWQKKK IAEMGPVQWL ATQKKAADKV
401  CFHHTICYFT EFLQNHCRSE VILEKWQKKK IAEMGPVQWL ATQKKAADKV
226  CFHHTICYFT EFLQNHCRSE VILEKWQKKK IAEMGPVQWL ATQKKAADKV

393  VFLLSNDVNS VCDGTCGKSE GSPSENSQDL FPLAFNLFCS DLRSQIHLHK
451  VFLLSNDVNS VCDGTCGKSE GSPSENSQDL FPLAFNLFCS DLRSQIHLHK
276  VFLLSNDVNS VCDGTCGKSE GSPSENSQDL FPLAFNLFCS DLRSQIHLHK

443  YVVVYFREID TKDDYNALSV CPKYHLMKDA TAFCAELLHV KQQVSAGKRS
501  YVVVYFREID TKDDYNALSV CPKYHLMKDA TAFCAELLHV KQQVSAGKRS
326  YVVVYFREID TKDDYNALSV CPKYHLMKDA TAFCAELLHV KQQVSAGKRS

493  QACHDGCCSL *
551  QACHDGCCSL *
376  QACHDGCCSL *
```

Figure 8

Northern Blot Expression Analysis of TH00-018 Necropsied Transgenic Founders

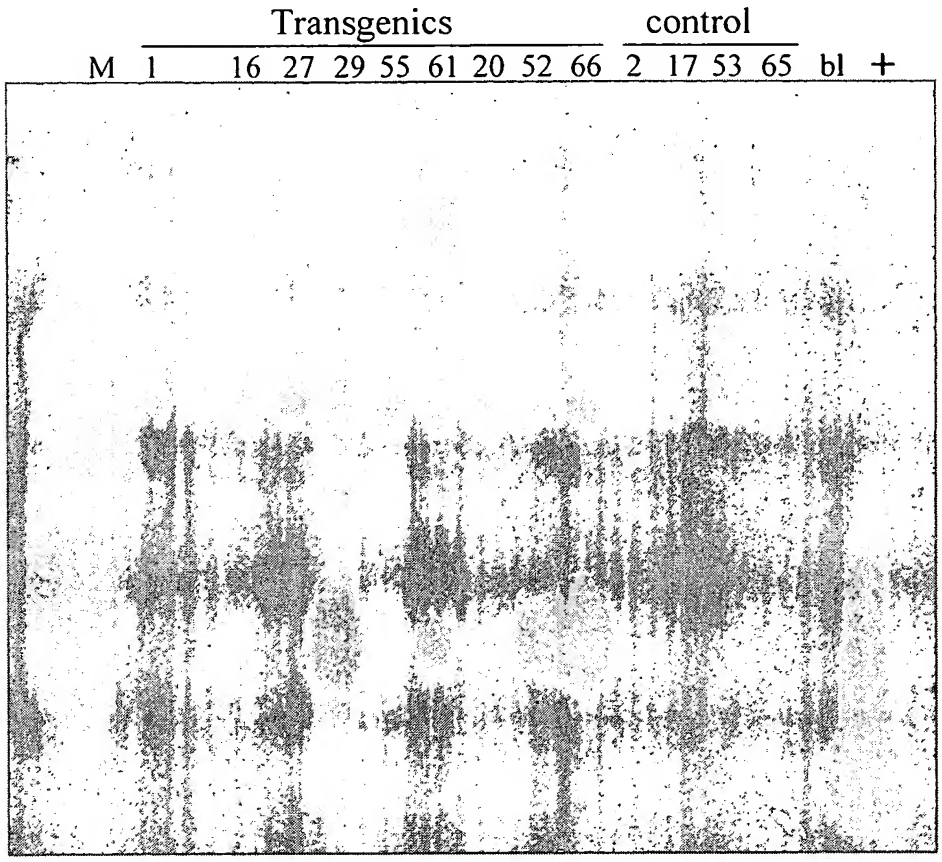

Figure 9

Northern Blot Expression Analysis of TH00-018
Hepatectomized Transgenic Founders

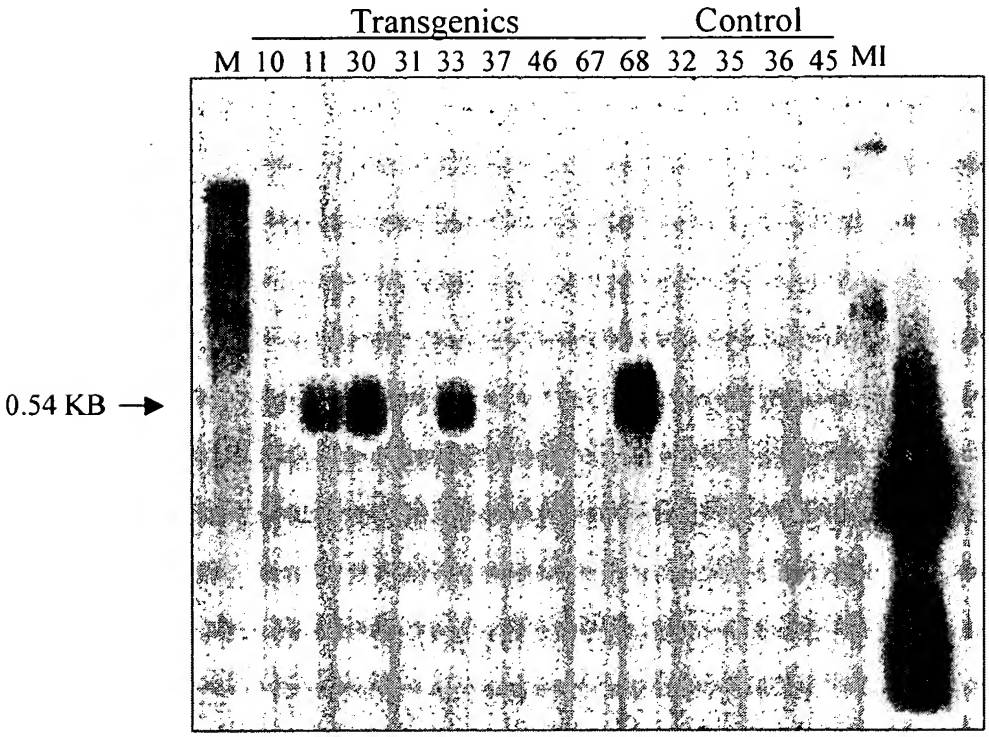

Figure 10

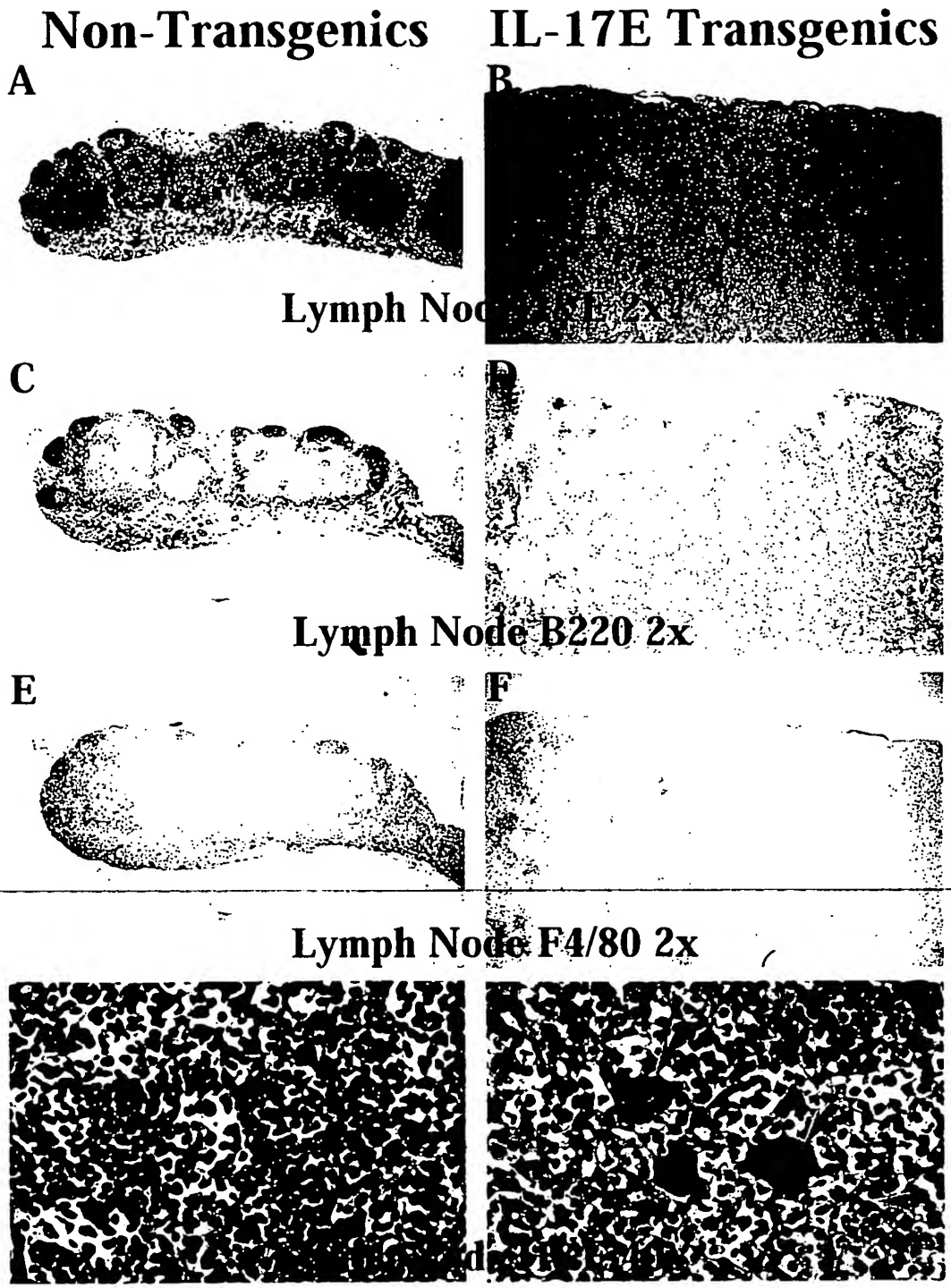
Non-Transgenics
IL-17E Transgenics
A
B
Lymph Noc
2x
C
D
Lymph Node B220 2x
E
F
Lymph Node F4/80 2x

Figure 11

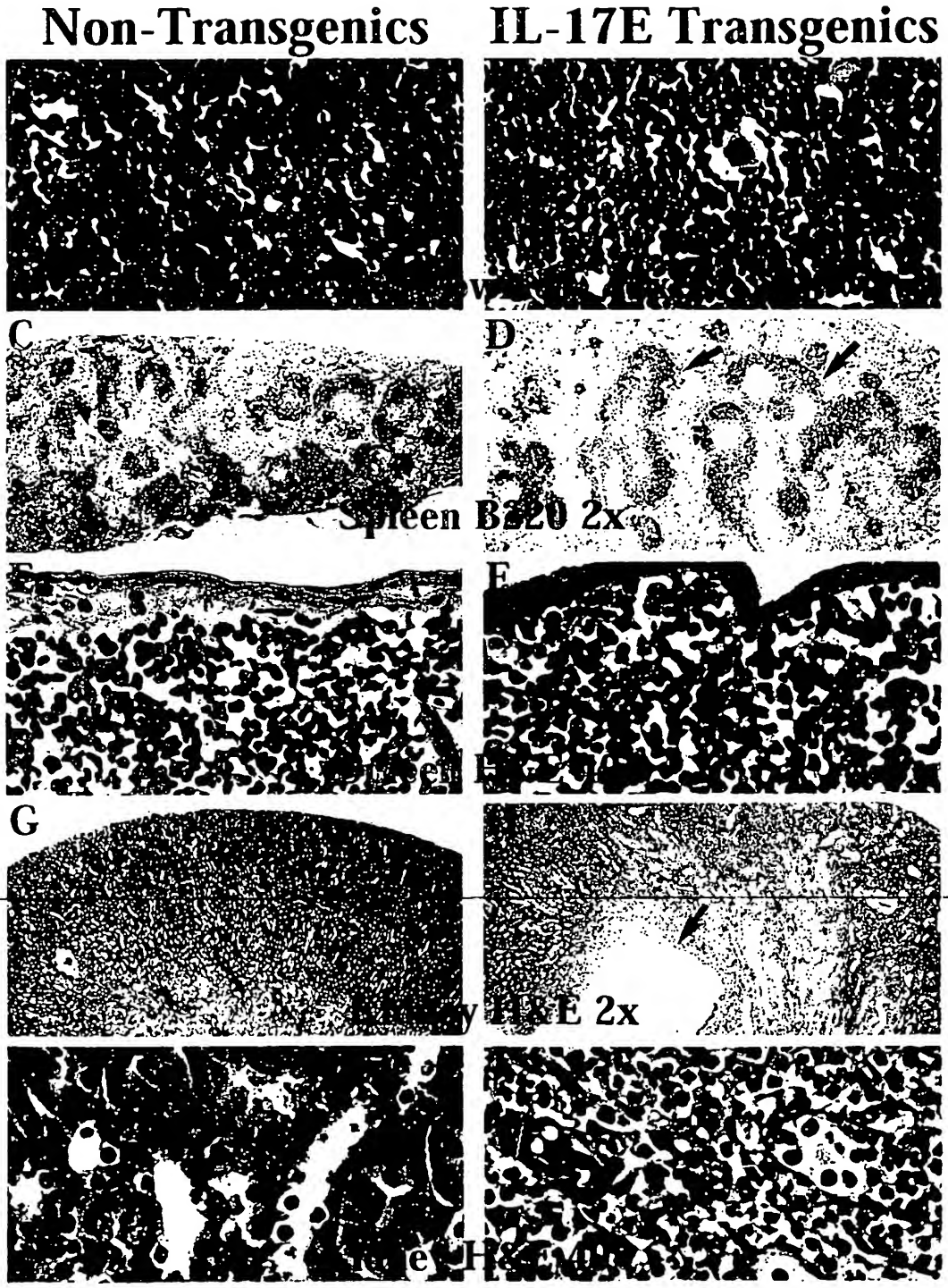
Non-Transgenics
IL-17E Transgenics
C
D
Spleen B220 2x
E
G
H&E 2x

Figure 12

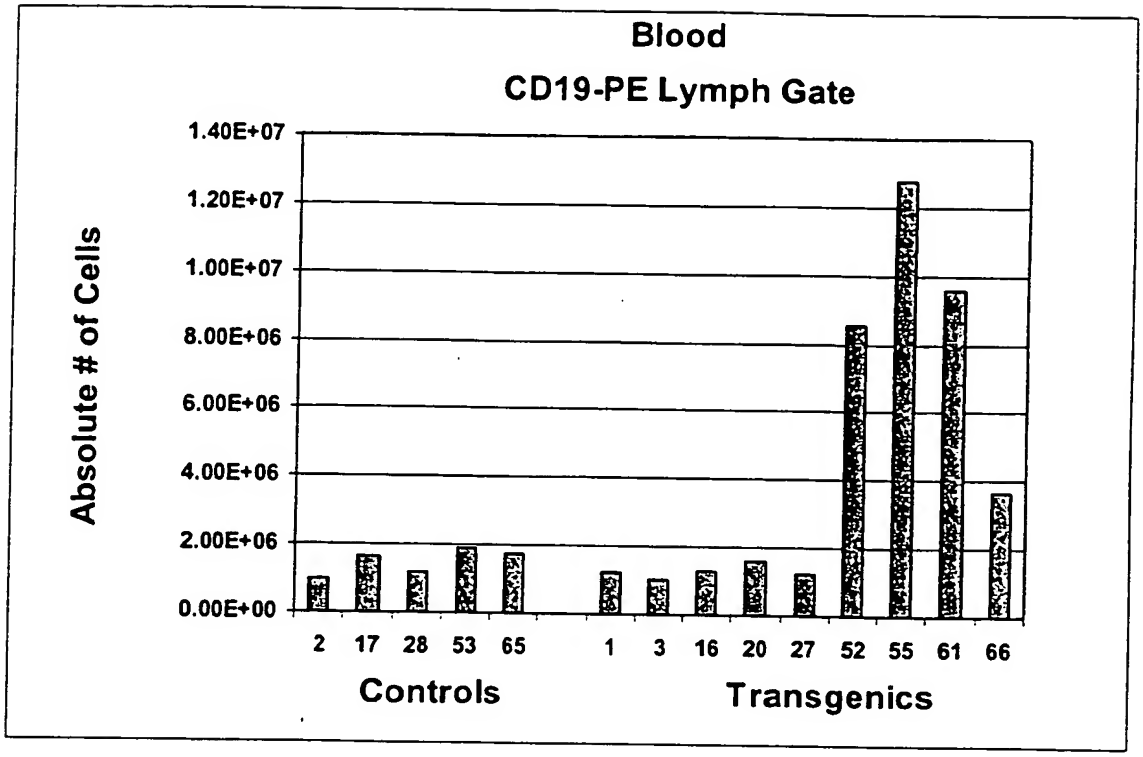
Blood
CD19-PE Lymph Gate
Absolute # of Cells
1.40E+07
1.20E+07
1.00E+07
8.00E+06
6.00E+06
4.00E+06
2.00E+06
0.00E+00
2 17 28 53 65
1 3 16 20 27 52 55 61 66
Controls
Transgenics

Figure 13

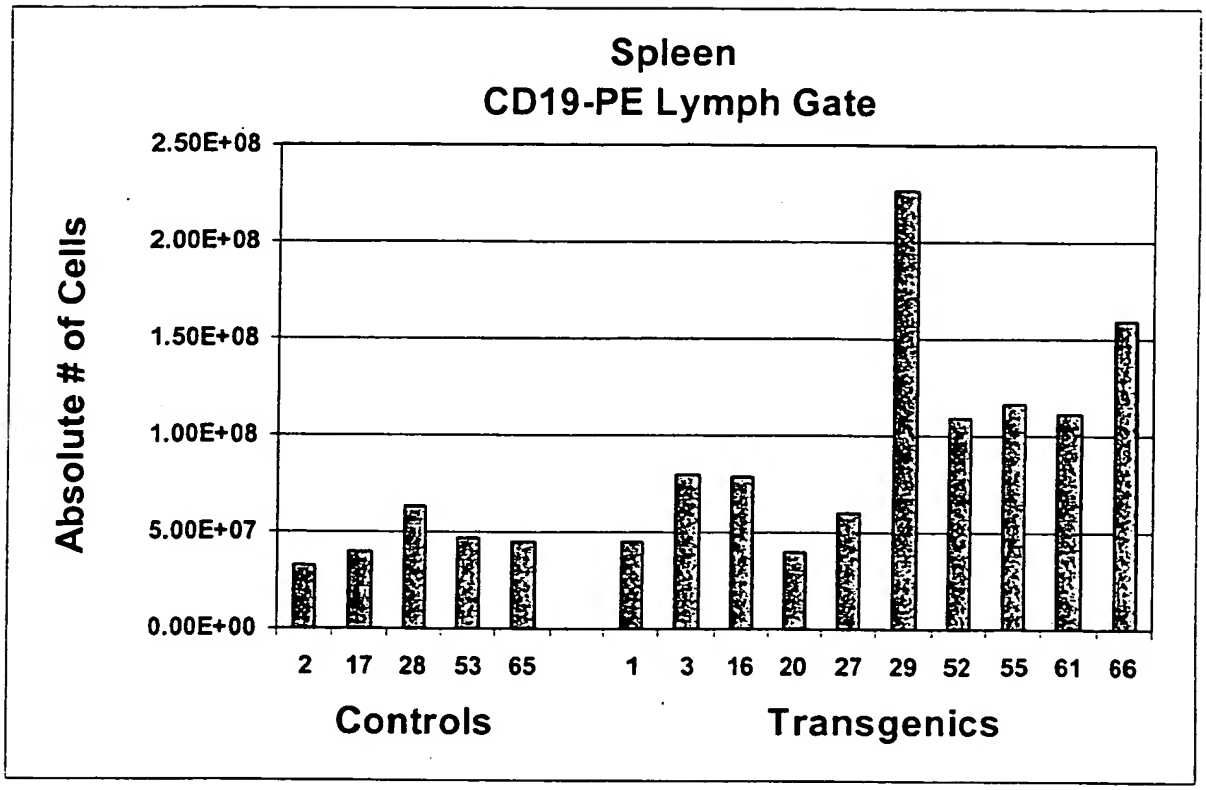
Spleen
CD19-PE Lymph Gate
Absolute # of Cells
2.50E+08
2.00E+08
1.50E+08
1.00E+08
5.00E+07
0.00E+00
2 17 28 53 65
1 3 16 20 27 29 52 55 61 66
Controls
Transgenics

Figure 14

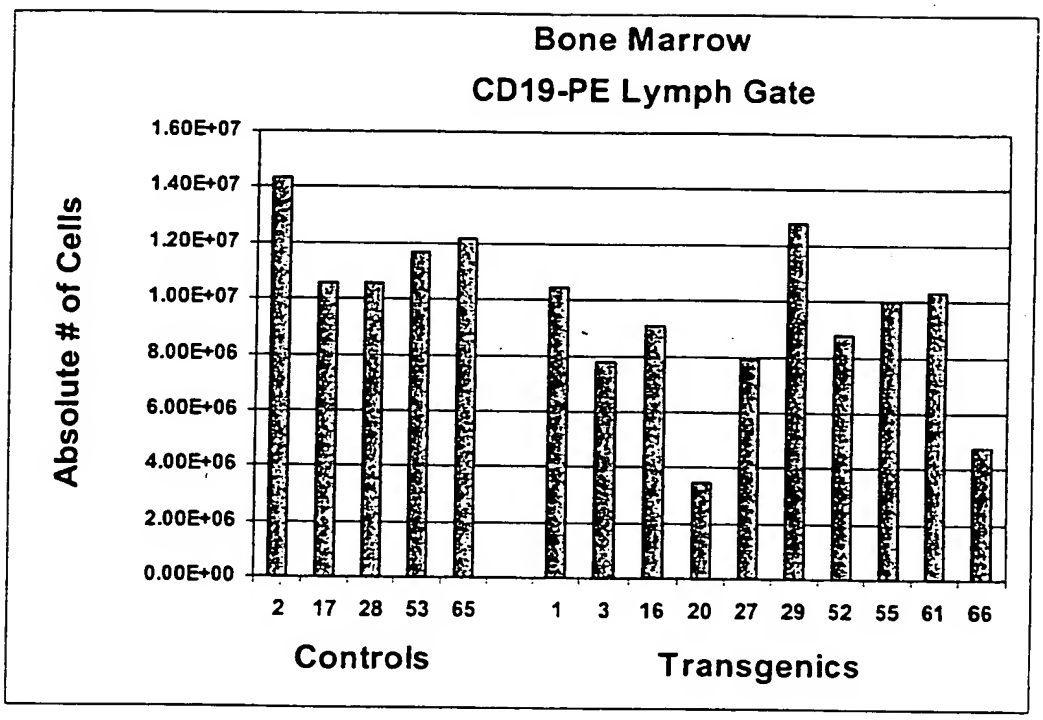
Bone Marrow
CD19-PE Lymph Gate
Absolute # of Cells
1.60E+07
1.40E+07
1.20E+07
1.00E+07
8.00E+06
6.00E+06
4.00E+06
2.00E+06
0.00E+00
2 17 28 53 65
1 3 16 20 27 29 52 55 61 66
Controls
Transgenics

Figure 15

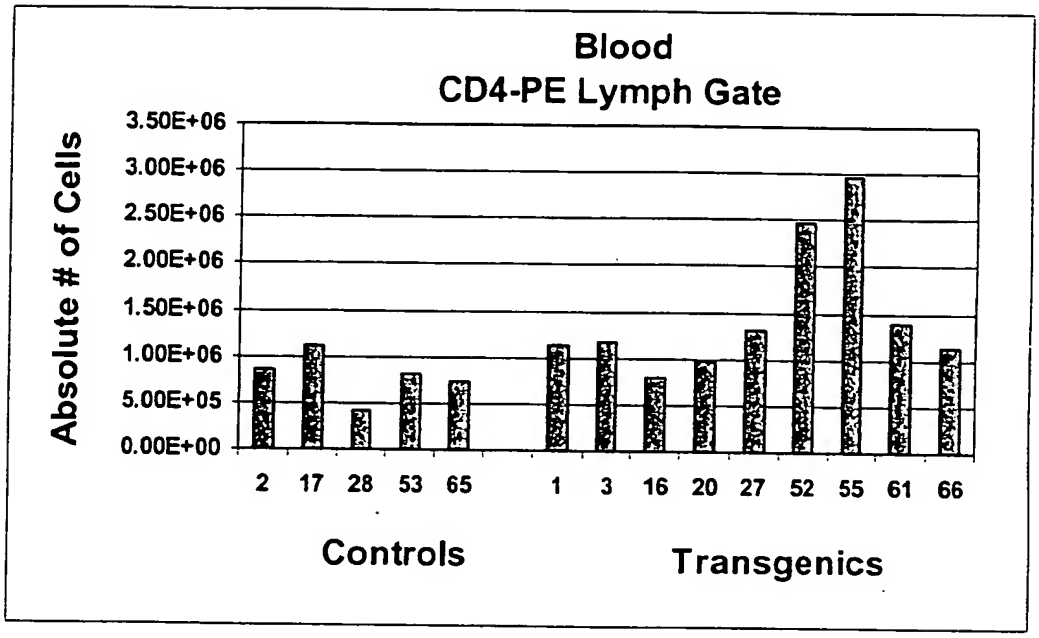
Blood
CD4-PE Lymph Gate
Absolute # of Cells
3.50E+06
3.00E+06
2.50E+06
2.00E+06
1.50E+06
1.00E+06
5.00E+05
0.00E+00
2 17 28 53 65
1 3 16 20 27 52 55 61 66
Controls
Transgenics

Figure 16

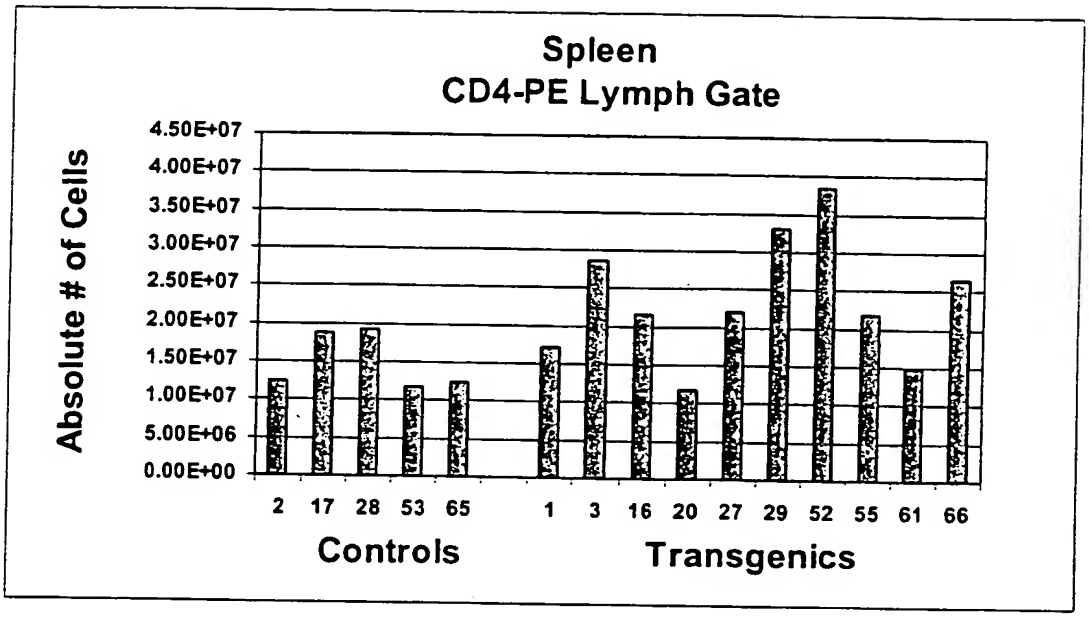
Spleen
CD4-PE Lymph Gate
Absolute # of Cells
4.50E+07
4.00E+07
3.50E+07
3.00E+07
2.50E+07
2.00E+07
1.50E+07
1.00E+07
5.00E+06
0.00E+00
2 17 28 53 65
1 3 16 20 27 29 52 55 61 66
Controls
Transgenics

Figure 17

CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

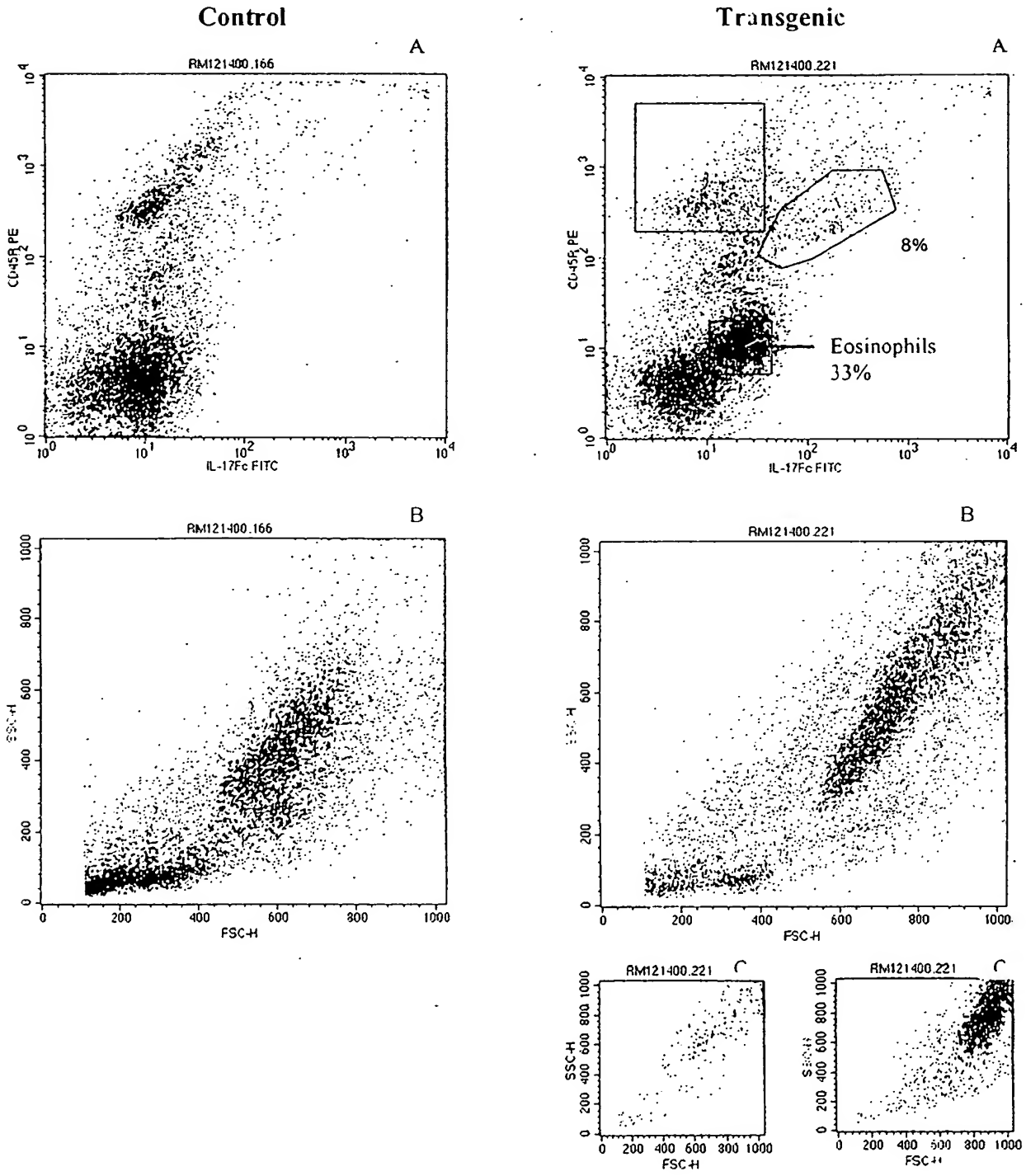

Figure 18

CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

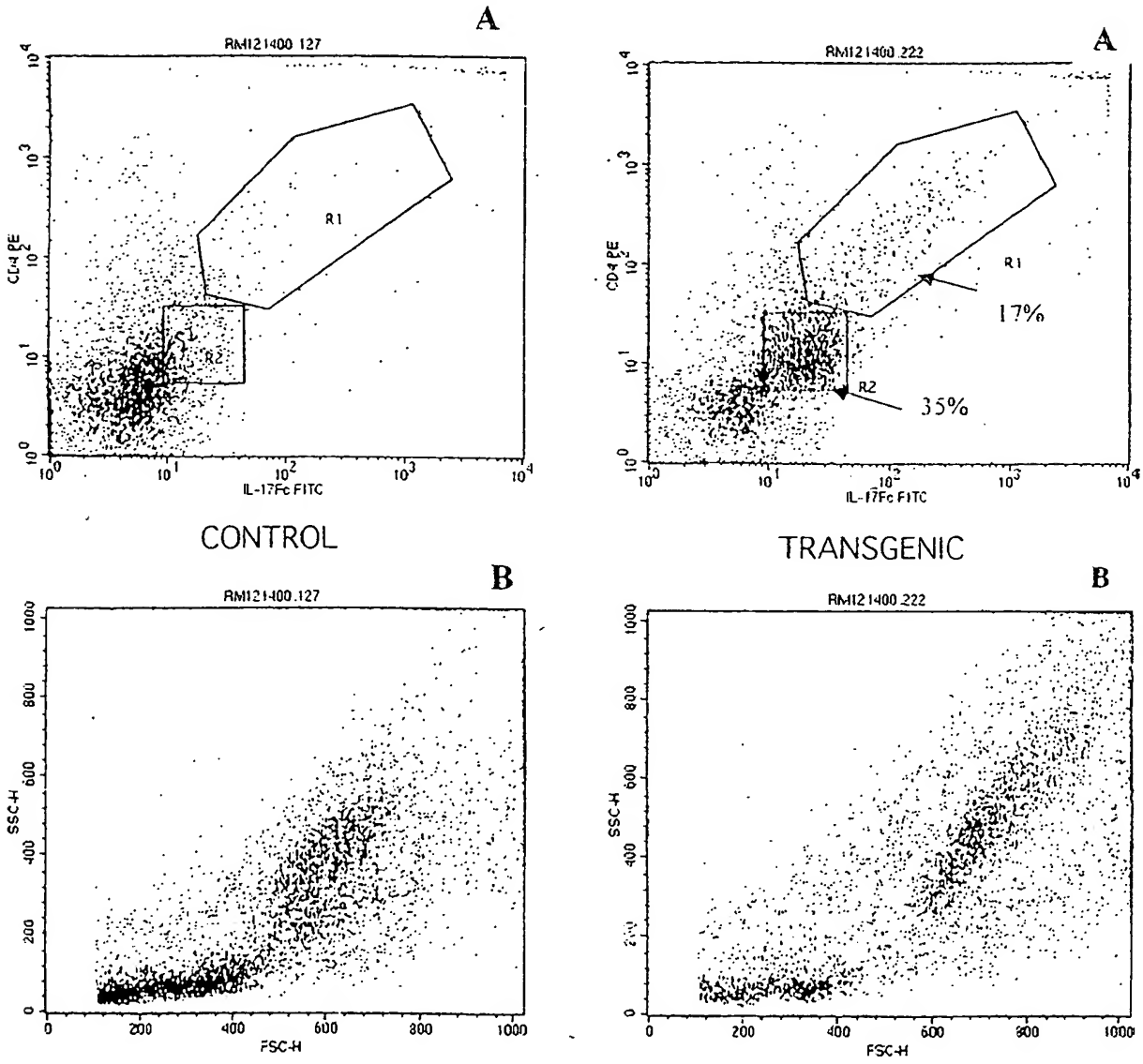

Figure 21

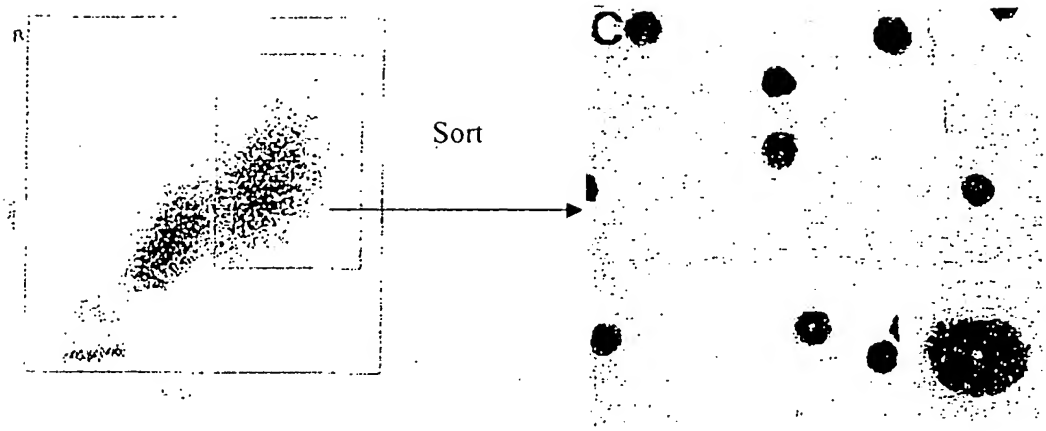

Figure 19

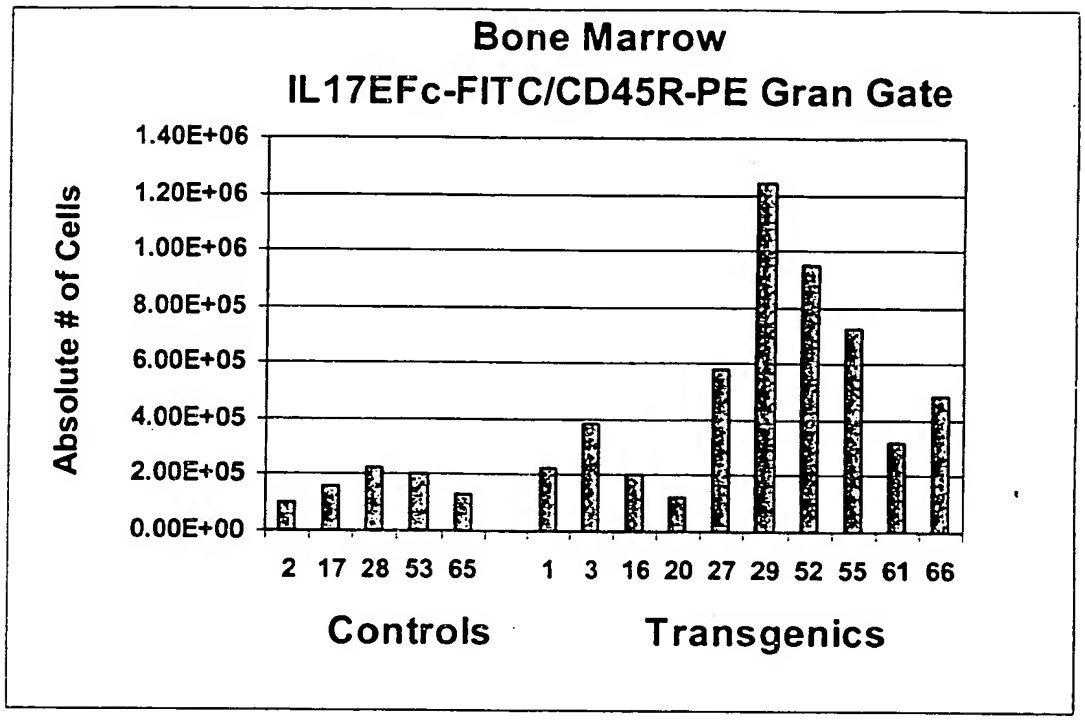
Bone Marrow
IL17EFc-FITC/CD45R-PE Gran Gate
Absolute # of Cells
1.40E+06
1.20E+06
1.00E+06
8.00E+05
6.00E+05
4.00E+05
2.00E+05
0.00E+00
2 17 28 53 65 1 3 16 20 27 29 52 55 61 66
Controls
Transgenics

Figure 20

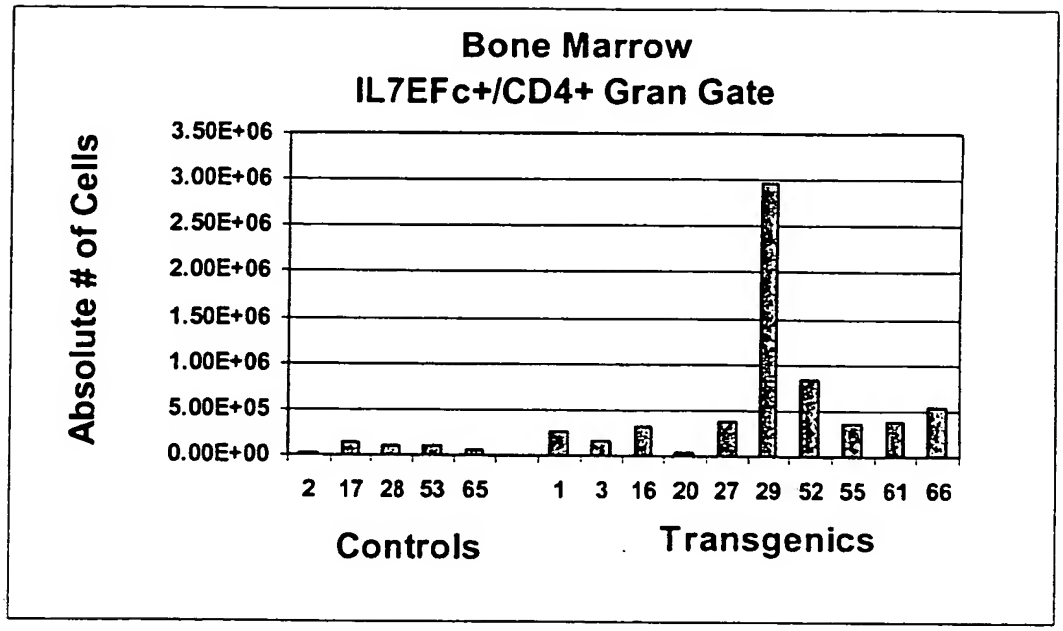
Bone Marrow
IL7EFc+/CD4+ Gran Gate
Absolute # of Cells
3.50E+06
3.00E+06
2.50E+06
2.00E+06
1.50E+06
1.00E+06
5.00E+05
0.00E+00
2 17 28 53 65 1 3 16 20 27 29 52 55 61 66
Controls
Transgenics

Figure 22

IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

1 ***MSLVLLSLAA LCRS***AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
51 EPVTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV
101 RCNYTEAFQT QTRPSGGKWT FSYIGFPVEL NTVYFIGAHN IPNANMNEDG
151 PSMSVNFTSP GCLDHIMKYK KKCVKAGSLW DPNITACKKN EETVEVNFTT
201 TPLGNRYMAL IQHSTIIGFS QVFEPHQKKQ TRASVVIPVT GDSEGATVQL
251 TPYFPTCGSD CIRHKGTVVL CPQTGVPFPL DNNKSKPGGW LPAAAEPKSC
301 DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED
351 PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK
401 CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK
451 GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG
501 NVFSCSVMHE ALHNHYTQKS LSLSPGK*

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1 ***MSLVLLSLAA LCRS***AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
51 EPVTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV
101 RLECSGAIMA RCDLNLLGSS DRSASASRAA GTAGVGHQTW LIFVVFVEGG
151 FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP
201 NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE
251 TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD
301 SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVPFPLDN NKSKPGGWLP
351 AAAEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV
401 VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD
451 WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP PSRDELTKNQ
501 VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV
551 DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK*